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Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2008; month=3; day=20; hr=15; min=6; sec=9; ms=551;]

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Application No: 10547447 Version No: 2.0

Input Set:

Output Set:

Started: 2008-02-29 16:55:52.428
Finished: 2008-02-29 16:55:58.398
Elapsed: 0 hr(s) 0 min(s) 5 sec(s) 970 ms
Total Warnings: 41
Total Errors: 35
No. of SeqIDs Defined: 59
Actual SeqID Count: 59

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (18)
W 402	Undefined organism found in <213> in SEQ ID (19)
W 402	Undefined organism found in <213> in SEQ ID (20)
W 402	Undefined organism found in <213> in SEQ ID (21)
W 402	Undefined organism found in <213> in SEQ ID (22)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)

Input Set:

Output Set:

Started: 2008-02-29 16:55:52.428
Finished: 2008-02-29 16:55:58.398
Elapsed: 0 hr(s) 0 min(s) 5 sec(s) 970 ms
Total Warnings: 41
Total Errors: 35
No. of SeqIDs Defined: 59
Actual SeqID Count: 59

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (25)
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W 213	Artificial or Unknown found in <213> in SEQ ID (26)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (26)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (29)
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W 213	Artificial or Unknown found in <213> in SEQ ID (31)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (31)
W 402	Undefined organism found in <213> in SEQ ID (34)
W 402	Undefined organism found in <213> in SEQ ID (35)
W 402	Undefined organism found in <213> in SEQ ID (36)
W 402	Undefined organism found in <213> in SEQ ID (37)

Input Set:

Output Set:

Started: 2008-02-29 16:55:52.428
Finished: 2008-02-29 16:55:58.398
Elapsed: 0 hr(s) 0 min(s) 5 sec(s) 970 ms
Total Warnings: 41
Total Errors: 35
No. of SeqIDs Defined: 59
Actual SeqID Count: 59

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (38)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (38)
W 213	Artificial or Unknown found in <213> in SEQ ID (39)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (39)
W 213	Artificial or Unknown found in <213> in SEQ ID (40)
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W 213	Artificial or Unknown found in <213> in SEQ ID (41)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (41)
W 213	Artificial or Unknown found in <213> in SEQ ID (42)
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E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (43)
W 213	Artificial or Unknown found in <213> in SEQ ID (44) This error has occurred more than 20 times, will not be displayed
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (44) This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Renz, Andreas
Heinz, Ernst
Abbadia, Amine
Domergue, Frederic
Zank, Thorsten

<120> METHOD FOR THE PRODUCTION OF POLYUNSATURATED FATTY ACIDS

<130> 12810-00119-US

<140> 10547447

<141> 2005-08-26

<150> PCT/EP2004/000771

<151> 2001-01-29

<150> DE 103 08 836.9

<151> 2003-02-27

<160> 59

<170> PatentIn version 3.5

<210> 1

<211> 849

<212> DNA

<213> *Caenorhabditis elegans*

<220>

<221> CDS

<222> (1)...(849)

<223> Acyl-CoA:lysophospholipid acyltransferase

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ttc att tta tat aac ata tcg aca gta tgc cac tac tat atg cggtt 96
Phe Ile Leu Tyr Asn Ile Ser Thr Val Cys His Tyr Tyr Met Arg Ile
20 25 30

tcg ttt tat tac ttc aca att tta ttg cat gga atg gaa gtt tgt gtt 144
Ser Phe Tyr Tyr Phe Thr Ile Leu Leu His Gly Met Glu Val Cys Val
35 40 45

aca atg atc cct tct tgg cta aat ggg aag ggt gct gat tac gtg ttt 192
Thr Met Ile Pro Ser Trp Leu Asn Gly Lys Gly Ala Asp Tyr Val Phe
50 55 60

cac tcg ttt ttc tat tgg tgt aaa tgg act ggt gtt cat aca aca gtc 240
His Ser Phe Phe Tyr Trp Cys Lys Trp Thr Gly Val His Thr Thr Val
65 70 75 80

tat gga tat gaa aaa aca caa gtt gaa ggt ccg gct gta gtt att tgt		288	
Tyr Gly Tyr Glu Lys Thr Gln Val Glu Gly Pro Ala Val Val Ile Cys			
85	90	95	
aat cat cag agt tct ctc gac att cta tcg atg gca tca atc tgg ccg		336	
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100	105	110	
aag aat tgt gtt gta atg atg aaa cga att ctt gcc tat gtt cca ttc		384	
Lys Asn Cys Val Val Met Met Lys Arg Ile Leu Ala Tyr Val Pro Phe			
115	120	125	
ttc aat ctc gga gcc tac ttt tcc aac aca atc ttc atc gat cga tat		432	
Phe Asn Leu Gly Ala Tyr Phe Ser Asn Thr Ile Phe Ile Asp Arg Tyr			
130	135	140	
aac cgt gaa cgt gcg atg gct tca gtt gat tat tgt gca tct gaa atg		480	
Asn Arg Glu Arg Ala Met Ala Ser Val Asp Tyr Cys Ala Ser Glu Met			
145	150	155	160
aag aac aga aat ctt aaa ctt tgg gta ttt ccg gaa gga aca aga aat		528	
Lys Asn Arg Asn Leu Lys Leu Trp Val Phe Pro Glu Gly Thr Arg Asn			
165	170	175	
cgt gaa gga ggg ttc att cca ttc aag aaa gga gca ttc aat att gca		576	
Arg Glu Gly Gly Phe Ile Pro Phe Lys Lys Gly Ala Phe Asn Ile Ala			
180	185	190	
gtt cgt gcg cag att ccc att att cca gtt gta ttc tca gac tat cgg		624	
Val Arg Ala Gln Ile Pro Ile Ile Pro Val Val Phe Ser Asp Tyr Arg			
195	200	205	
gat ttc tac tca aag cca ggc cga tat ttc aag aat gat gga gaa gtt		672	
Asp Phe Tyr Ser Lys Pro Gly Arg Tyr Phe Lys Asn Asp Gly Glu Val			
210	215	220	
gtt att cga gtt ctg gat gcg att cca aca aaa ggg ctc act ctt gat		720	
Val Ile Arg Val Leu Asp Ala Ile Pro Thr Lys Gly Leu Thr Leu Asp			
225	230	235	240
gac gtc agc gag ttg tct gat atg tgt cgg gac gtt atg ttg gca gcc		768	
Asp Val Ser Glu Leu Ser Asp Met Cys Arg Asp Val Met Leu Ala Ala			
245	250	255	
tat aag gaa gtt act cta gaa gct cag caa cga aat gcg aca cgg cgt		816	
Tyr Lys Glu Val Thr Leu Glu Ala Gln Gln Arg Asn Ala Thr Arg Arg			
260	265	270	
gga gaa aca aaa gac ggg aag aaa tct gag taa		849	
Gly Glu Thr Lys Asp Gly Lys Lys Ser Glu			
275	280		

<210> 2
<211> 282
<212> PRT

<213> Caenorhabditis elegans

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Met Glu Asn Phe Trp Ser Ile Val Val Phe Phe Leu Leu Ser Ile Leu
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Phe Ile Leu Tyr Asn Ile Ser Thr Val Cys His Tyr Tyr Met Arg Ile
20 25 30

Ser Phe Tyr Tyr Phe Thr Ile Leu Leu His Gly Met Glu Val Cys Val
35 40 45

Thr Met Ile Pro Ser Trp Leu Asn Gly Lys Gly Ala Asp Tyr Val Phe
50 55 60

His Ser Phe Phe Tyr Trp Cys Lys Trp Thr Gly Val His Thr Thr Val
65 70 75 80

Tyr Gly Tyr Glu Lys Thr Gln Val Glu Gly Pro Ala Val Val Ile Cys
85 90 95

Asn His Gln Ser Ser Leu Asp Ile Leu Ser Met Ala Ser Ile Trp Pro
100 105 110

Lys Asn Cys Val Val Met Met Lys Arg Ile Leu Ala Tyr Val Pro Phe
115 120 125

Phe Asn Leu Gly Ala Tyr Phe Ser Asn Thr Ile Phe Ile Asp Arg Tyr
130 135 140

Asn Arg Glu Arg Ala Met Ala Ser Val Asp Tyr Cys Ala Ser Glu Met
145 150 155 160

Lys Asn Arg Asn Leu Lys Leu Trp Val Phe Pro Glu Gly Thr Arg Asn
165 170 175

Arg Glu Gly Gly Phe Ile Pro Phe Lys Lys Gly Ala Phe Asn Ile Ala
180 185 190

Val Arg Ala Gln Ile Pro Ile Ile Pro Val Val Phe Ser Asp Tyr Arg
195 200 205

Asp Phe Tyr Ser Lys Pro Gly Arg Tyr Phe Lys Asn Asp Gly Glu Val
210 215 220

Val Ile Arg Val Leu Asp Ala Ile Pro Thr Lys Gly Leu Thr Leu Asp
225 230 235 240

Asp Val Ser Glu Leu Ser Asp Met Cys Arg Asp Val Met Leu Ala Ala
245 250 255

Tyr Lys Glu Val Thr Leu Glu Ala Gln Gln Arg Asn Ala Thr Arg Arg
260 265 270

Gly Glu Thr Lys Asp Gly Lys Lys Ser Glu
275 280

<210> 3
<211> 849
<212> DNA
<213> *Caenorhabditis elegans*

<220>
<221> CDS
<222> (1)..(849)
<223> Acyl-CoA:lysophospholipid acyltransferase

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Met Glu Asn Phe Trp Ser Ile Val Val Phe Phe Leu Leu Ser Ile Leu
1 5 10 15

ttc att tta tat aac ata tcg aca gta tgc cac tac tat atg cggtt 96
Phe Ile Leu Tyr Asn Ile Ser Thr Val Cys His Tyr Tyr Met Arg Ile
20 25 30

tcg ttt tat tac ttc aca att tta ttg cat gga atg gaa gtt tgt gtt 144
Ser Phe Tyr Tyr Phe Thr Ile Leu Leu His Gly Met Glu Val Cys Val
35 40 45

aca atg atc cct tct tgg cta aat ggg aag ggt gct gat tac gtg ttt 192
Thr Met Ile Pro Ser Trp Leu Asn Gly Lys Gly Ala Asp Tyr Val Phe
50 55 60

cac tcg ttt ttc tat tgg tgt aaa tgg act ggt gtt cat aca aca gtc 240
His Ser Phe Phe Tyr Trp Cys Lys Trp Thr Gly Val His Thr Thr Val
65 70 75 80

tat gga tat gaa aaa aca caa gtt gaa ggt ccg gct gta gtt att tgt 288
Tyr Gly Tyr Glu Lys Thr Gln Val Glu Gly Pro Ala Val Val Ile Cys
85 90 95

aat cat cag agt tct ctc gac att cta tcg atg gca tca atc tgg ccg 336

Asn His Gln Ser Ser Leu Asp Ile Leu Ser Met Ala Ser Ile Trp Pro			
100	105	110	
aag aat tgt gtt gta atg atg aaa cga att ctt gcc tat gtt cca ttc			384
Lys Asn Cys Val Val Met Met Lys Arg Ile Leu Ala Tyr Val Pro Phe			
115	120	125	
ttc aat ctc gga gcc tac ttt tcc aac aca atc ttc atc gat cga tat			432
Phe Asn Leu Gly Ala Tyr Phe Ser Asn Thr Ile Phe Ile Asp Arg Tyr			
130	135	140	
aac cgt gaa cgt gcg atg gct tca gtt gat tat tgt gca tct gaa atg			480
Asn Arg Glu Arg Ala Met Ala Ser Val Asp Tyr Cys Ala Ser Glu Met			
145	150	155	160
aag aac aga aat ctt aaa ctt tgg gta tct ccg gaa gga aca aga aat			528
Lys Asn Arg Asn Leu Lys Leu Trp Val Ser Pro Glu Gly Thr Arg Asn			
165	170	175	
cgt gaa gga ggg ttc att cca ttc aag aaa gga gca ttc aat att gca			576
Arg Glu Gly Gly Phe Ile Pro Phe Lys Lys Gly Ala Phe Asn Ile Ala			
180	185	190	
gtt cgt gcg cag att ccc att att cca gtt gta ttc tca gac tat cgg			624
Val Arg Ala Gln Ile Pro Ile Ile Pro Val Val Phe Ser Asp Tyr Arg			
195	200	205	
gat ttc tac tca aag cca ggc cga tat ttc aag aat gat gga gaa gtt			672
Asp Phe Tyr Ser Lys Pro Gly Arg Tyr Phe Lys Asn Asp Gly Glu Val			
210	215	220	
gtt att cga gtt ctg gat gcg att cca aca aaa ggg ctc act ctt gat			720
Val Ile Arg Val Leu Asp Ala Ile Pro Thr Lys Gly Leu Thr Leu Asp			
225	230	235	240
gac gtc agc gag ttg tct gat atg tgt cgg gac gtt atg ttg gca gcc			768
Asp Val Ser Glu Leu Ser Asp Met Cys Arg Asp Val Met Leu Ala Ala			
245	250	255	
tat aag gaa gtt act cta gaa gct cag caa cga aat gcg aca cgg cgt			816
Tyr Lys Glu Val Thr Leu Glu Ala Gln Gln Arg Asn Ala Thr Arg Arg			
260	265	270	
gga gaa aca aaa gac ggg aag aaa tct gag taa			849
Gly Glu Thr Lys Asp Gly Lys Lys Ser Glu			
275	280		

<210> 4
<211> 282
<212> PRT
<213> Caenorhabditis elegans

<400> 4

Met Glu Asn Phe Trp Ser Ile Val Val Phe Phe Leu Leu Ser Ile Leu			
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Phe Ile Leu Tyr Asn Ile Ser Thr Val Cys His Tyr Tyr Met Arg Ile
20 25 30

Ser Phe Tyr Tyr Phe Thr Ile Leu Leu His Gly Met Glu Val Cys Val
35 40 45

Thr Met Ile Pro Ser Trp Leu Asn Gly Lys Gly Ala Asp Tyr Val Phe
50 55 60

His Ser Phe Phe Tyr Trp Cys Lys Trp Thr Gly Val His Thr Thr Val
65 70 75 80

Tyr Gly Tyr Glu Lys Thr Gln Val Glu Gly Pro Ala Val Val Ile Cys
85 90 95

Asn His Gln Ser Ser Leu Asp Ile Leu Ser Met Ala Ser Ile Trp Pro
100 105 110

Lys Asn Cys Val Val Met Met Lys Arg Ile Leu Ala Tyr Val Pro Phe
115 120 125

Phe Asn Leu Gly Ala Tyr Phe Ser Asn Thr Ile Phe Ile Asp Arg Tyr
130 135 140

Asn Arg Glu Arg Ala Met Ala Ser Val Asp Tyr Cys Ala Ser Glu Met
145 150 155 160

Lys Asn Arg Asn Leu Lys Leu Trp Val Ser Pro Glu Gly Thr Arg Asn
165 170 175

Arg Glu Gly Gly Phe Ile Pro Phe Lys Lys Gly Ala Phe Asn Ile Ala
180 185 190

Val Arg Ala Gln Ile Pro Ile Ile Pro Val Val Phe Ser Asp Tyr Arg
195 200 205

Asp Phe Tyr Ser Lys Pro Gly Arg Tyr Phe Lys Asn Asp Gly Glu Val
210 215 220

Val Ile Arg Val Leu Asp Ala Ile Pro Thr Lys Gly Leu Thr Leu Asp
225 230 235 240

Asp Val Ser Glu Leu Ser Asp Met Cys Arg Asp Val Met Leu Ala Ala

245

250

255

Tyr Lys Glu Val Thr Leu Glu Ala Gln Gln Arg Asn Ala Thr Arg Arg

260

265

270

Gly Glu Thr Lys Asp Gly Lys Lys Ser Glu

275

280

<210> 5

<211> 849

<212> DNA

<213> *Caenorhabditis elegans*

<220>

<221> CDS

<222> (1)..(849)

<223> Acyl-CoA:lysophospholipid acyltransferase

<400> 5

atg gag aac ttc tgg tcg atc gtc gtg ttt ttt cta ctc tca att ctc 48
Met Glu Asn Phe Trp Ser Ile Val Val Phe Phe Leu Leu Ser Ile Leu
1 5 10 15

ttc att tta tat aac ata tcg aca gta tgc cac tac tat gtg cgg att 96
Phe Ile Leu Tyr Asn Ile Ser Thr Val Cys His Tyr Tyr Val Arg Ile
20 25 30

tcg ttt tat tac ttc aca att tta ttg cat gga atg gaa gtt tgt gtt 144
Ser Phe Tyr Tyr Phe Thr Ile Leu Leu His Gly Met Glu Val Cys Val
35 40 45

aca atg atc cct tct tgg cta aat ggg aag ggt gct gat tac gtg ttt 192
Thr Met Ile Pro Ser Trp Leu Asn Gly Lys Gly Ala Asp Tyr Val Phe
50 55 60

cac tcg ttt ttc tat tgg tgt aaa tgg act ggt gtt cat aca aca gtc 240
His Ser Phe Phe Tyr Trp Cys Lys Trp Thr Gly Val His Thr Thr Val
65 70 75 80

tat gga tat gaa aaa aca caa gtt gaa ggt ccg gct gta gtt att tgt 288
Tyr Gly Tyr Glu Lys Thr Gln Val Glu Gly Pro Ala Val Val Ile Cys
85 90 95

aat cat cag agt tct ctc gac att cta tcg atg gca tca atc tgg ccg 336
Asn His Gln Ser Ser Leu Asp Ile Leu Ser Met Ala Ser Ile Trp Pro
100 105 110

aag aat tgt gtt gta atg atg aaa cga att ctt gcc tat gtt cca ttc 384
Lys Asn Cys Val Val Met Met Lys Arg Ile Leu Ala Tyr Val Pro Phe
115 120 125

ttc aat ctc gga gcc tac ttt tcc aac aca atc ttc atc gat cga tat		432
Phe Asn Leu Gly Ala Tyr Phe Ser Asn Thr Ile Phe Ile Asp Arg Tyr		
130	135	140
 aac cgt gaa cgt gcg atg gct tca gtt gat tat tgt gca tct gaa atg		480
Asn Arg Glu Arg Ala Met Ala Ser Val Asp Tyr Cys Ala Ser Glu Met		
145	150	155
 aag aac aga aat ctt aaa ctt tgg gta ttt ccg gaa gga aca aga aat		528
Lys Asn Arg Asn Leu Lys Leu Trp Val Phe Pro Glu Gly Thr Arg Asn		
165	170	175
 cgt gaa gga ggg ttc att cca ttc aag aaa gga gca ttc aat att gca		576
Arg Glu Gly Gly Phe Ile Pro Phe Lys Lys Gly Ala Phe Asn Ile Ala		
180	185	190
 gtt cgt gcg cag att ccc att att cca gtt gta ttc tca gac tat cg		624
Val Arg Ala Gln Ile Pro Ile Ile Pro Val Val Phe Ser Asp Tyr Arg		
195	200	205
 gat ttc tac tca aag cca ggc cga tat ttc aag aat gat gga gaa gtt		672
Asp Phe Tyr Ser Lys Pro Gly Arg Tyr Phe Lys Asn Asp Gly Glu Val		
210	215	220
 gtt att cga gtt ctg gat gcg att cca aca aaa ggg ctc act ctt gat		720
Val Ile Arg Val Leu Asp Ala Ile Pro Thr Lys Gly Leu Thr Leu Asp		
225	230	235
 gac gtc agc gag ttg tct gat atg tgt cg gac gtt atg ttg gca gcc		768
Asp Val Ser Glu Leu Ser Asp Met Cys Arg Asp Val Met Leu Ala Ala		
245	250	255
 tat aag gaa gtt act cta gaa gct cag caa cga aat gcg aca cg cgt		816
Tyr Lys Glu Val Thr Leu Glu Ala Gln Gln Arg Asn Ala Thr Arg Arg		
260	265	270
 gga gaa aca aaa gac ggg aag aaa tct gag taa		